```
OM of: US-09-092-297-17 to: EST:*     out_format : pfs

Date: Jan 22, 2000  3:26 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-1998 Compugen Ltd.

Command line parameters:
-MODEL-frame+_p2n.model
-Q~/cgn2_1/USPTO_spool/US09092297/runat_20012000_151103_15802/app_query.fasta.1
-DB=EST -QFMT=fastap -SUFFIX=merjan202000.rst -GAPOP=4.500
-GAPEXT=.050 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=60.000 -XGAPEXO=60.000
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=oligo
-TRANS=human40.cd1 -LIST=45 -DOCALIGN=200 -THR_SCORE=quality
-THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=1000000 -USER=US09092297 -NCPU=6 -ICPU=3 -NO_XLPXX -WAIT
-THREADS=1

Sr    Information block:
Q~    US-09-092-297-17
Query length: 117
Database: EST:*
Database sequences: 4089388
Database length: 1713965092
Search time (sec): 1255.040000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000
WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000
```

score_list:

Sequence	Strd	Orig	ZScore	EScore	Len	Documentation
gb_est15:AA456370	+	82.00	1565.10	1.9e-78	412	AA456370 aa14e02.r1 Soares_NhHM
gb_est29:AI572169	+	24.00	452.16	1.8e-16	275	AI572169 te37e06.x1 Soares_NhHM
gb_est11:AA195677	-	16.00	294.23	1.1e-07	475	AA195677 zr32h04.s1 Soares_NhHM
gb_est14:F20995	-	8.00	160.76	3.11	403	F20995 HSPD05444 HM3 Homo sapie
gb_gss3:AQ034057	-	8.00	139.49	47.58	531	AQ034057 1(3)03576 Drosophila m
gb_gss8:AQ581989	+	8.00	137.81	59.00	667	AQ581989 RPCI-11-460D1.TV RPCI-
gb_est11:M89022	-	7.00	120.57	538.22	508	M89022 CEl14C2 Chris Martin sor
gb_est1:T03295	-	7.00	121.73	463.95	434	T03295 FB9P8 Fetal brain, Strat
gb_est1:T38570	-	7.00	123.64	363.42	335	T38570 ES010407J S. cerevisiae
gb_est2:R09194	-	7.00	127.26	228.67	205	R09194 yf22g01.s1 Soares fetal
gb_est2:R15249	-	7.00	121.02	508.19	478	R15249 yf89c04.r1 Soares infant
gb_est2:T68381	-	7.00	123.72	359.32	331	T68381 yc41f05.r1 Stratagene 1:
gb_est2:H12824	-	7.00	123.61	364.44	336	H12824 yj14e08.r1 Soares placen
gb_est3:R48084	-	7.00	121.22	495.14	465	R48084 yj45c02.r1 Soares breast
gb_est3:R67627	-	7.00	121.08	504.18	474	R67627 yj69c11.s1 Soares breast
gr :R72741	-	7.00	124.35	331.61	307	R72741 yj9lall.r1 Soares breast
3:R78139	+	7.00	122.06	444.76	415	R78139 yl80g10.r1 Soares placen
gb_est3:R80111	-	7.00	121.01	509.19	479	R80111 y195f05.r1 Soares breast
gb_est4:H28322	-	7.00	124.75	315.12	288	H28322 yl60f10.r1 Soares breast
gb_est4:T76317	-	7.00	123.66	362.39	334	T76317 11095 Lambda-PRL2 Arabi
gb_est5:H69509	-	7.00	121.89	454.87	425	H69509 yu71f10.r1 Weizmann Olfa
gb_est5:H74591	-	7.00	124.47	326.46	299	H74591 19 Deletion-treated Bras
gb_est5:N37337	-	7.00	122.19	437.68	408	N37337 18564 Lambda-PRL2 Arabid
gb_est5:N42067	-	7.00	123.02	393.02	364	N42067 yw94g07.r1 Soares placen
gb_est6:N70110	-	7.00	122.24	434.65	405	N70110 za53h09.s1 Soares fetal
gb_est6:W01207	-	7.00	120.76	525.22	495	W01207 za59b07.r1 Soares fetal
gb_est7:W17541	-	7.00	123.66	478.05	448	W17541 mb62g09.r1 Soares mouse
gb_est8:AA045641	+	7.00	123.66	362.39	334	AA045641 zk83b12.s1 Soares_preg
gb_est8:W14179	-	7.00	121.53	476.04	446	W14179 mb38b08.r1 Soares pregna
gb_est9:AA105850	-	7.00	119.36	628.73	599	AA105850 mm02f10.r1 Stratagene
gb_est9:AA119287	-	7.00	122.96	396.07	367	AA119287 mp78g09.r1 Soares 2NbM
gb_est9:C19615	-	7.00	121.32	489.12	459	C19615 C19615 Rice panicle at t
gb_est9:C22082	-	7.00	125.28	294.44	268	C22082 C22082 Miyagawa-wase sat
gb_est10:AA141336	-	7.00	119.44	622.79	593	AA141336 CK01837.5prime CK Dros
gb_est10:AA162738	-	7.00	121.38	485.09	455	AA162738 mn43a02.r1 Beddington
gb_est10:AA163025	-	7.00	121.15	500.16	470	AA163025 mr28b09.r1 Soares mous
gb_est10:AA181054	-	7.00	119.22	640.60	611	AA181054 zp66g12.s1 Stratagene
gb_est10:AA186122	+	7.00	120.81	522.22	492	AA186122 mu56e12.r1 Stratagene
gb_est11:AA200013	+	7.00	121.16	499.16	469	AA200013 mu02a02.r1 Soares mous

seq_name: gb_est15:AA456370

seq_documentation_block:
gb_est11:AA208890	+	+	7.00	125.28	294.44	268	AA208890 mw76a02.r1 Soares m
gb_est11:AA210174	+	+	7.00	122.65	412.34	383	AA210174 mu39f12.r1 Soares 2
gb_est11:AA213286	+	+	7.00	120.12	570.15	540	AA213286 mu73c09.r1 Strataga
gb_est11:AA217016	+	+	7.00	120.79	523.22	493	AA217016 mu04f02.r1 Soares m
gb_est11:AA217432	+	+	7.00	121.68	466.97	437	AA217432 mu94f11.r1 Soares m
gb_gss9:AQ601263	+	+	7.00	121.58	473.02	443	AQ601263 HS_2093_A1_G11_T7C

seq_name: gb_est15:AA456370

seq_documentation_block:
```
LOCUS       AA456370      412 bp   mRNA        EST       06-JUN-1997
DEFINITION  aa14e02.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:813242
            5', mRNA sequence.
ACCESSION   AA456370
NID         g2178946
VERSION     AA456370.1  GI:2178946
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 412)
AUTHORS     Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
            Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
            WashU-Merck EST Project 1997
TITLE       Unpublished (1997)
JOURNAL     On Sep 1, 1995 this sequence version replaced.
COMMENT
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 398.
FEATURES             Location/Qualifiers
     source          1..412
                     /organism="Homo sapiens"
                     /db_xref="GDB:6044152"
                     /db_xref="taxon:9606"
                     /map="21"
                     /clone="IMAGE:813242"
                     /clone_lib="Soares_NhHMPu_S1"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; Equal amounts of plasmid DNA from three
                     normalized libraries (melanocyte 2NbHM, pregnant uterus
                     NbHPU, and fetal heart NbHH19W) were mixed and ss circles
                     were made in vitro. Following HAP purification, this DNA
                     was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from pools of
                     5,000 clones made from the same 3 libraries. The pools
                     consisted of I.M.A.G.E. clones 260232-265223,
                     340488-345479, and 484488-489479."
BASE COUNT       88 a       116 c       119 g       89 t
ORIGIN
```

alignment_scores:
Quality:	82.00	Length:	82
Ratio:	1.000	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

alignment_block:
US-09-092-297-17 x AA456370

Align seg 1/1 to: AA456370 from: 1 to: 412

```
36   ProMetThrProTyrLeuMetLeuGlnProHisLysArgCysGlyAs   52
     ||||||||||||||||||||||||||||||||||||||||||||||
35   CCCATGACTCCTTACCTGATGCTGTCGCAGCCACACAAGAGATGTGGGGA   84

52   pLysPheTyrAspProLeuGlnHisCysCysTyrAspAspAlaValValP   69
     |||||||||||||||||||||||||||||||||||||||||||||||
85   CAAGTTCTACGACCCCCTCCAGCACTGTTCCTATGATGATGCCGTCGTGC 134

69   roLeuAlaArgThrGlnThrCysGlyAsnCysThrProHisArgValCysPhe  85
     ||||||||||||||||||||||||||||||||||||||||||||||
135  CCTTGGCCAGGACCCAGACGTGTGGAAACTGCACCTTCAGACGTGCTTT  184

86   GluGlnCysProTrpThrPheMetValLysLeuIleAsnGlnAsnCy  102
     ||||||||||||||||||||||||||||||||||||||||||||||
185  GAGCAGTGCCCTGGACCTTCATGGTGAAGCTGATAAACCAGAACTG  234

102  sAspSerAlaAargThrSerAspAspArgLeuCysArgSerValSer  117
     ||||||||||||||||||||||||||||||||||||||||||||||
235  CGACTCAGCCGGCGAACCTCGGATGACAGGCTTTGTCGCAGTGTCAC  280
```

seq_name: gb_est29:AI572169

seq.documentation_block:
LOCUS   AI572169   275 bp   mRNA   EST   13-APR-1999
DEFINITION   te37e06.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2088898
              3', mRNA sequence.
ACCESSION   AI572169
NID   g4535543
VERSION   AI572169.1 GI:4535543
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
              Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 275)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   On Jun 2, 1997 this sequence version replaced gi:2152659.

FEATURES   Location/Qualifiers
     source   1..275
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="21"
                     /clone="IMAGE:2088898"
                     /clone_lib="Soares_NhHMPu_S1"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; Equal amounts of plasmid DNA from three
                     normalized libraries (melanocyte 2NbHM, pregnant uterus
                     NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                     were made in vitro. Following HAP purification, this DNA
                     was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from pools of
                     5,000 clones made from the same 3 libraries. The pools
                     consisted of I.M.A.G.E. clones 260232-265223,
                     340488-345479, and 484488-489479."

BASE COUNT   58 a   77 c   56 g   84 t
ORIGIN

alignment_scores:
        Quality: 24.00   Length: 24
        Ratio: 1.000   Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-092-297-17 x AI572169

Align seg 1/1 to: AI572169 from: 1 to: 275

```
41   LeuMetLeuCysGlnProHisLysArgCysGlyAspLysPheTyrAspPr   57
     ||||||||||||||||||||||||||||||||||||||||||||||
180  CTGATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCC  229

57   oLeuGlnHisCysCysTyrAsp  64
     ||||||||||||||||||||||
230  CCTGCAGCACTGTTCCTATGAT  251
```

seq_name: gb_est11:AA195677

seq.documentation_block:
LOCUS   AA195677   475 bp   mRNA   EST   19-MAY-1997
DEFINITION   zr32h04.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665143
              3', mRNA sequence.
ACCESSION   AA195677
NID   g1785355
VERSION   AA195677.1 GI:1785355
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
              Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 475)
AUTHORS   Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
              Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
              Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
              Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
              Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
              Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.,
              and Marra,M.
TITLE   Generation and analysis of 280,000 human expressed sequence tags
JOURNAL   Genome Res. 6 (9), 807-828 (1996)
MEDLINE   97044478
COMMENT   On Dec 18, 1996 this sequence version replaced gi:1734281.

FEATURES   Location/Qualifiers
     source   1..475
                     /organism="Homo sapiens"
                     /db_xref="GDB:542175"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:665143"
                     /clone_lib="Soares_NhHMPu_S1"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; Equal amounts of plasmid DNA from three
                     normalized libraries (melanocyte 2NbHM, pregnant uterus
```

NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."

BASE COUNT    109 a    122 c    134 g    108 t    2 others
ORIGIN

alignment_scores:
```
      Quality: 16.00   Length: 16
      Ratio: 1.000   Gaps: 0
Percent Similarity: 100.000   Percent Identity: 100.000
```
alignment_block:
US-09-092-297-17 x AA195677/rev

Align seg 1/1 to reverse of: AA195677 from: 1 to: 475

```
102 CysAspSerAlaArgThrSerAspAspArgLeuCysArgSerValSer 117
    |||||||||||||||||||||||||||||||||||||||||||||||
460 TGCGACTCAGCCCGGACCTCGGATGACAGAGCGTTTGTCGCAGTGTCAGC 413
```

seq_name: gb_est14:F20995

```
LOCUS       F20995       403 bp       mRNA       EST       17-MAY-1999
DEFINITION  HSPD05444 HM3 Homo sapiens cDNA clone 034-X4-13, mRNA sequence.
ACCESSION   F20995
NID         g2060171
VERSION     F20995.1 GI:2060171
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 403)
  AUTHORS   Lanfranchi,G., Muraro,T., Caldara,F., Pacchioni,B., Pallavicini,A.,
            Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G.
  TITLE     Identification of 4370 expressed sequence tags from a
            3'-end-specific cDNA library of human skeletal muscle by DNA
            sequencing and filter hybridization
  JOURNAL   Genome Res. 6 (1), 35-42 (1996)
  MEDLINE   9676048
COMMENT     On Dec 30, 1996 this sequence version replaced gi:1529536.
```

Contact: Valle G.
CRIBI Biotechnology Centre
University of Padua
Via Trieste 75, 35121 Padua, Italy
ABI Chromatograms and other information are available on WWW at
http://grup.bio.unipd.it;

```
FEATURES             Location/Qualifiers
     source          1..403
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /sex="female"
                     /clone="HM3"
                     /clone_lib="HM3"
                     /clone="034-X4-13"
                     /tissue_type="pectoral muscle (after mastectomy)"
                     /note="Vector: pcDNAII (Invitrogen); Site_1: BstXI;
                     Site_2: NotI; The library was constructed by G.
                     Lanfranchi. This library is not subtracted nor normalized.
                     The first strand cDNA was primed with a biotinylated
                     oligo-dT-NotI primer
                     (5'-biotin-AACCGGCGTCGACGGGCGCGCCTTTTTTTTTTTTTTTTTT-3'). The
                     ds cDNA was sonicated and size-selected in the range
                     350-550 bp. The 3' specific fragments were selected by
                     streptavidin coated magnetic beads, ligated to
                     non-palindromic BstXI adapters, NotI digested and
                     directionally cloned into BstXI-NotI cut pcDNAII vector."
```

BASE COUNT   105 a   97 c   98 g   97 t   6 others
ORIGIN

alignment_scores:
```
      Quality:    9.00              Length:   9
      Ratio:      1.000              Gaps:     0
Percent Similarity: 100.000     Percent Identity: 100.000
```
alignment_block:
US-09-092-297-17 x F20995/rev

Align seg 1/1 to reverse of: F20995/rev ...

```
 66 AlaValAlaValProLeuAlaLeuAlaArgThrGln 74
    |||||||||||||||||||||||||||||||||||
297 GCCGTTGTGCCTCCTCCAAGAACACAA 271
```

seq_name: gb_gss3:AQ034057

```
LOCUS       AQ034057       531 bp       DNA       GSS       07-JUL-1998
DEFINITION  1(3)03576 Drosophila melanogaster P lethal line Drosophila
            melanogaster genomic Sequence recovered from Both 5' and 3' ends of
            P element, genomic survey sequence.
ACCESSION   AQ034057
NID         g3293677
VERSION     AQ034057.1 GI:3293677
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea;
            Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 531)
  AUTHORS   Spradling,A.C., Stern,D., Beaton,A., Rehm,E.J., Laverty,T.,
            Mozden,N., Misra,S. and Rubin,G.M.
  TITLE     The BDGP gene disruption project: Single P element insertions
            mutating 30% of Drosophila autosomal genes
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Gerald Rubin
            Berkeley Drosophila Genome Project
            University of California, Berkeley
            LSA Building, Berkeley, Berkeley, CA 94720-3200, USA
            Fax: 5106439947
            Email: gerry@fruitfly.berkeley.edu

            Sequence recovery method was inverse PCR.

            Sequence orientation is forward strand relative to 5' end of P
            element

            The P element insertion position is base 105 in the 531 bases. This
            insertion position refers to the first base of the 8 base target
            recognition sequence.

            This sequence is also known as STS Dm0281

            Class: transposon-tagged.
FEATURES             Location/Qualifiers
     source          1..531
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="Drosophila melanogaster P lethal line"
                     /note="Inverse PCR was performed on Drosophila
                     melanogaster strains each of which contains a single P
                     transposable element insertion that is thought to cause
                     either lethality or sterility. The resultant fragment for
                     each strain was directly sequenced to determine the
                     genomic sequence at the site of insertion. Details of the
                     protocols used can be found at
                     http://fruitfly.berkeley.edu/p_disrupt/inverse_pcr.html."
```

BASE COUNT   123 a   117 c   146 g   145 t
ORIGIN

alignment_scores:
    Quality: 8.00   Length: 8
    Ratio: 1.000   Gaps: 0
Percent Similarity: 100.000   Percent Identity: 100.000

seq_name: gb_gss8:AQ581989

Align seg 1/1 to: AQ034057 from: 1 to: 531

alignment_block:
US-09-092-297-17 x AQ034057   ...
52 TCTCATGGTGCACCTGTGTAGCCACCG 75
   |||||||||||||||||||||||||||
29 SerHisGlyAlaProValAlaPro 36

s   ocumentation_block:
Lo~S   AQ581989   667 bp   DNA   GSS   07-JUN-1999
DEFINITION RPCI-11-460D1.TV RPCI-11 Homo sapiens genomic clone RPCI-11-460D1,
           genomic survey sequence.
ACCESSION AQ581989
NID   g5009099
VERSION   AQ581989.1 GI:5009099
KEYWORDS   GSS.
SOURCE   human.
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
           Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 667)
AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
           Venter,J.C.
TITLE   Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
           Map Building
JOURNAL   Unpublished (1997)
COMMENT   Contact: Shaying Zhao, William Nierman, Mark Adams
           Department of Eukaryotic Genomics
           The Institute for Genomic Research
           9712 Medical Center Dr., Rockville, MD 20850
           Tel: 301 838 0200
           Fax: 301 838 0208
           Email: hbeetigr.org
           Clones are derived from the human BAC library RPCI-11. For BAC
           library availability, please contact Pieter de Jong
           (pieter@dejong.med.buffalo.edu). Clones may be purchased from
           BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
           Research Genet cs (info@resgen.com). BAC end search page:
           http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
           Seq primer: T7
           Class: BAC ends.
FEATURES   Location/Qualifiers
   source 1..667
           /organism="Homo sapiens"
           /db_xref="GDB:7676328"
           /db_xref="taxon:9606"
           /clone="RPCI-11-460D1"
           /clone_lib="RPCI-11"
           /sex="Male"
           /cell_type="lymphocytes"
           /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
           RPCI11 Human Male BAC Library"
BASE COUNT   163 a   113 c   136 g   255 t
ORIGIN

alignment_scores:
    Quality: 8.00   Length: 8
    Ratio: 1.000   Gaps: 0
Percent Similarity: 100.000   Percent Identity: 100.000

---

alignment_block:
US-09-092-297-17 x AQ581989   ...

Align seg 1/1 to: AQ581989 from: 1 to: 667

338 TGTATTTCTAGGCTACTGTGCTCC 361
    |||||||||||||||||||||||||
22 CysIleSerArgLeuLeuCysSer 29

seq_name: gb_est1:M89022

seq_documentation_block:
LOCUS   M89022   508 bp   mRNA   EST   02-DEC-1992
DEFINITION CEL14C2 Chris Martin sorted cDNA library Caenorhabditis elegans
           cDNA clone cm14c2 5' similar to flavin-containing monooxygenase
           homologous peptide, mRNA sequence.
ACCESSION M89022
NID   g275523
VERSION   M89022.1 GI:275523
KEYWORDS   EST.
SOURCE   Caenorhabditis elegans.
ORGANISM   Caenorhabditis elegans
           Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
           Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 508)
AUTHORS   Waterston,R., Martin,C., Craxton,M., Huynh,C., Coulson,A.,
           Hillier,L., Durbin,R.K., Green,P., Shownkeen,R., Halloran,N.,
           Hawkins,T., Wilson,R., Berks,M., Du,Z., Thomas,K., Thierry-Mieg,J.
           and Sulston,J.
TITLE   A survey of expressed genes in Caenorhabditis elegans
JOURNAL   Nature Genet. 1, 114-123 (1992)
MEDLINE   93250982
COMMENT   Contact: Waterston R.H.(USA) and Sulston J.E.(UK)
           (USA) Dept. of Genetics or (UK)
           (USA) Washington Univ. School of Medicine or (UK) MRC Laboratory of
           Molecular Biology
           Box 8232,4566 Scott Ave.,St. Louis,MI 63110,USA,or,Hills
           Road,Cambridge CB2 2QH,UK
           Tel: (USA) (314)3627072 or (UK) (0223)248011
           Fax: (USA) (314)3624137 or (UK) (0223)402008
           Email: rw@nematode.wustl.edu or jes@mrc-lmba.cambridge.ac.uk
           single read.
FEATURES   Location/Qualifiers
   source 1..508
           /organism="Caenorhabditis elegans"
           /strain="Bristol N2"
           /db_xref="taxon:6239"
           /clone="cm14c2"
           /clone_lib="Chris Martin sorted cDNA library"
           /lab_host="MC1061"
           /note="Vector: lambdaphage SHLX2; Mixed stage
           hermaphrodite cDNA library. Partially normalized by
           successively picking groups of clones that didn't
           hybridize to previously picked clones. Vector: lambdaphage
           SHLX2 (Lipshitz, D.H. et al., Gene 88:25-36 (1990)) Host:
           MC1061"
BASE COUNT   138 a   106 c   130 g   130 t   4 others
ORIGIN

alignment_scores:
    Quality: 7.00   Length: 7
    Ratio: 1.000   Gaps: 0
Percent Similarity: 100.000   Percent Identity: 100.000

Align seg 1/1 to: M89022 from: 1 to: 508

110 AspArgLeuCysArgSerVal 116

```
seq_name: gb_est1:T03295

          !|||||||||||||||||||||||||||
     343  GATCGAATATGCCGATCAGTG 363

seq_documentation_block:
LOCUS       T03295          434 bp    mRNA              EST       14-FEB-1997
DEFINITION  FB9F8 Fetal brain, Stratagene Homo sapiens cDNA clone FB9F8 3'end,
            mRNA sequence.
ACCESSION   T03295
NID         g314535
VERSION     T03295.1    GI:314535
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 434)
AUTHORS     Khan,A.S., Wilcox,A.S., Polymeropoulos,M.H., Hopkins,J.A.,
            Stevens,T.J., Robinson,M., Orpana,A.K. and Sikela,J.M.
TITLE       Single pass sequencing and physical and genetic mapping of human
            cDNAs
JOURNAL     Nature Genet. 2, 180-185 (1992)
MEDLINE     94258200
COMMENT     On Sep 21, 1992 this sequence version replaced gi:279432.

            Contact: Sikela JM
            Department of Pharmacology
            University of Colorado Health Sciences Center
            Box C236, 4200 E. 9th Ave, Denver CO 80262-0236
            Tel: 3032708637
            Fax: 3032707097
            Email: nikki@tally.uchsc.edu
            Seq primer: -21M13 Universal.
FEATURES             Location/Qualifiers
     source          1..434
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):86940"
                     /db_xref="GDB:DOS3055E"
                     /db_xref="taxon:9606"
                     /clone="FB9F8"
                     /clone_lib="Fetal brain, Stratagene"
                     /note="Vector: Lambda ZAP II; The FB library (catalog
                     #937201, Stratagene) was constructed by directional
                     cloning and oligo d(T)-priming in Lambda ZAP II phage
                     utilizing mRNA from a 17 week human fetus (total brain)."
BASE COUNT     92 a     121 c     116 g     100 t     5 others
ORIGIN

alignment_scores:
        Quality:              7.00              Length:           7
        Ratio:                1.000             Gaps:             0
Percent Similarity: 100.000        Percent Identity: 100.000

alignment_block:
US-09-092-297-17 x T03295

Align seg 1/1  to: T03295  from: 1  to: 434

       26  LeuLeuCysSerHisGlyAla  32
           !||||||||||||||||||||
      137  CTCCTCTGCTCCACGTGCC  157

seq_name: gb_est1:T38570

seq_documentation_block:
LOCUS       T38570          335 bp    mRNA              EST       11-JAN-1995
DEFINITION  EST104073 S. cerevisiae strain X2180-1A Saccharomyces cerevisiae
            cDNA 3' end, mRNA sequence.
ACCESSION   T38570
NID         g622387
VERSION     T38570.1    GI:622387
```

```
KEYWORDS    EST.
SOURCE      baker's yeast.
ORGANISM    Saccharomyces cerevisiae
            Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
            Saccharomycetaceae; Saccharomyces.
REFERENCE   1  (bases 1 to 335)
AUTHORS     Weinstock,K.
TITLE       Saccharomyces cerevisiae cDNAs
JOURNAL     Unpublished (1995)
COMMENT     Other_ESTs: TC539
            Contact: Weinstock,K. and Venter,J.C.
            The Institute for Genomic Research
            932 Clopper Rd, Gaithersburg, MD 20878
            Tel: 3018699056
            Fax: 3018699423
            Email: tdbinfo@tigr.org
            For clone availability please contact the TIGR Database
            (tdbinfo@tigr.org)
            Seq primer: M13-21.
FEATURES             Location/Qualifiers
     source          1..335
                     /organism="Saccharomyces cerevisiae"
                     /strain="X2180-1A"
                     /db_xref="taxon:4932"
                     /clone_lib="S. cerevisiae strain X2180-1A"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT     99 a     74 c     61 g     101 t
ORIGIN

alignment_scores:
        Quality:              7.00              Length:           7
        Ratio:                1.000             Gaps:             0
Percent Similarity: 100.000        Percent Identity: 100.000

alignment_block:
US-09-092-297-17 x T38570/rev

Align seg 1/1  to reverse of: T38570  from: 1  to: 335

       67  ValValProLeuAlaArgThr  73
           !||||||||||||||||||||
      147  GTTGTCCCTCTCCGGAGGACC  127

seq_name: gb_est2:R09194

seq_documentation_block:
LOCUS       R09194          205 bp    mRNA              EST       05-APR-1995
DEFINITION  yf22c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone
            IMAGE:127632 3', mRNA sequence.
ACCESSION   R09194
NID         g761117
VERSION     R09194.1    GI:761117
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 205)
AUTHORS     Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
TITLE       The WashU-Merck EST Project
JOURNAL     Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
```

Left record

```
Email: est@watson.wustl.edu
Insert Size: 978
High qality sequence stops: 196 Source: IMAGE Consortium, LLNL This
clone is available royalty-free through LLNL ; contact the IMAGE
Consortium (info@image.llnl.gov) for further information.
Insert Length: 978    Std Error: 0.00
Seq primer: -21m13
High quality sequence stop: 196.
FEATURES             Location/Qualifiers
source          1..205
                /organism="Homo sapiens"
                /db_xref="GDB:479793"
                /map="4"
                /db_xref="taxon:9606"
                /clone="IMAGE:127632"
                /clone_lib="Soares fetal liver spleen 1NFLS"
                /sex="male"
                /dev_stage="20 week-post conception fetus"
                /lab_host="DH10B (ampicillin resistant)"
                /note="Organ: liver and spleen; Vector: pT73D (Pharmacia)
                with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                1st strand cDNA was primed with a Pac I - oligo(dT) primer
                [5' AACTGGAAGAATTAATTAAAGAGTCTTTTTTTTTTTTTTTTTT 3'],
                double-stranded cDNA was ligated to Eco RI adaptors
                (Pharmacia), digested with Pac I and cloned into the Pac I
                and Eco RI sites of the modified pT73 vector. Library
                went through one round of normalization. Library
                constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT     45 a    56 c    41 g    63 t
ORIGIN
```

```
alignment_scores:
       Quality:         7.00
       Ratio:           1.000
Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
US-09-092-297-17 x R09194

Align seg 1/1 to: R09194    from: 1   to: 205   ..

   31 GlyAlaProValAlaProMet 37
      |||||||||||||||||||||
  169 GGGGCCCTGTTGCACCCATG 189
```

```
seq_name: gb_est2:R15249

  documentation_block:
L  R15249               478 bp    mRNA            EST      13-APR-1995
DEFINITION  yf89o04.r1 Soares infant brain 1NIB Homo sapiens cDNA clone
            IMAGE:29761 5' similar to gb:X06661_cds1 CALBINDIN (HUMAN);, mRNA
            sequence.
ACCESSION   R15249
NID         g769522
VERSION     R15249.1   GI:769522
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 478)
AUTHORS     Hillier,L., Clark,N., Dubuque,T., Elliston,R., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
TITLE       The WashU-Merck EST Project
JOURNAL     Unpublished (1995)
COMMENT     On Sep 21, 1992 this sequence version replaced gi:276431.

            Contact: Wilson RK
            Washington University School of Medicine
```

Right record

```
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 310
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: M13Rpl
High quality sequence stop: 310.
FEATURES             Location/Qualifiers
source          1..478
                /organism="Homo sapiens"
                /db_xref="GDB:402108"
                /db_xref="taxon:9606"
                /clone="IMAGE:29761"
                /clone_lib="Soares infant brain 1NIB"
                /sex="female"
                /dev_stage="73 days post natal"
                /lab_host="DH10B (ampicillin resistant)"
                /note="Organ: whole brain; Vector: Lafmid BA; Site_1: Not
                I; Site_2: Hind III; 1st strand cDNA was primed with a Not
                I - oligo(dT) primer [5'
                AACTGGAAGAATTCCGCGGCCGCAGGAATTTTTTTTTTTTTTTTTTT 3'];
                double-stranded cDNA was ligated to Hind III adaptors
                (Pharmacia), digested with Not I and directionally cloned
                into the Not I and Hind III sites of the Lafmid BA vector.
                Library went through one round of normalization. Library
                constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT     112 a    131 c    126 g    103 t    6 others
ORIGIN
```

```
alignment_scores:
       Quality:         7.00
       Ratio:           1.000
Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
US-09-092-297-17 x R15249

Align seg 1/1 to: R15249    from: 1   to: 478   ..

   69 ProLeuAlaArgThrGlnThr 75
      |||||||||||||||||||||
   98 CCCCTCCGCCGCGGACACAGACA 118
```

```
seq_name: gb_est2:T68381

seq_documentation_block:
LOCUS       T68381             331 bp    mRNA            EST      22-FEB-1995
DEFINITION  yc41f05.r1 Stratagene liver (#937224) Homo sapiens cDNA clone
            IMAGE:83265 5' similar to gb:M14219 BONE PROTEOGLYCAN II PRECURSOR
            (HUMAN);, mRNA sequence.
ACCESSION   T68381
NID         g679529
VERSION     T68381.1   GI:679529
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 331)
AUTHORS     Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
            Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
            Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
            Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
            Rohling,T., Schellenberg,K., Soares,M.B., Tan,F., Therry-Meg,J.,
            Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
            and Marra,M.
TITLE       Generation and analysis of 280,000 human expressed sequence tags
JOURNAL     Genome Res. 6 (9), 807-828 (1996)
MEDLINE     97044478
```

COMMENT   On Oct 24, 1994 this sequence version replaced.

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 480
High qality sequence stops: 218 Source: IMAGE Consortium, LLNL This
clone is available royalty-free through LLNL ; contact the IMAGE
Consortium (info@image.llnl.gov) for further information.
Insert Length: 480   Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 218.

FEATURES   Location/Qualifiers
     source   1..331
                     /organism="Homo sapiens"
                     /db_xref="GDB:500322"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:83265"
                     /clone_lib="Stratagene liver (#937224)"
                     /sex="male"
                     /dev_stage="49 years old"
                     /lab_host="SOLR cells (kanamycin resistant)"
                     /note="Organ: liver; Vector: pBluescript SK; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
                     Oligo dT. Hepatectomy from normal male caucasian. Average
                     insert size: 1.1 kb; Uni-ZAP XR Vector; -5' adaptor
                     sequence: 5' GAATTCGGCACGAG 3' -3' adaptor sequence: 5'
                     CTCGAGTTTTTTTTTTTTTTTTTTTTT 3'."

BASE COUNT   86 a   76 c   78 g   89 t   2 others
ORIGIN

alignment_scores:
        Quality: 7.00   Length: 7
        Ratio: 1.000   Gaps: 0
Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
US-09-092-297-17 x T68381/rev   .

Align seg 1/1 to reverse of: T68381   from: 1 to: 331

         40 TyrIleuMetLeuCysGlnPro 46
            |||||||||||||||||||||||
        187 TACTTAAYGCTCTGCCAGCCC 167

s   ame: gb_est3:H12824

seq_documentation_block:
LOCUS   H12824   336 bp   mRNA   EST   27-JUN-1995
DEFINITION yj14e08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone
            IMAGE:148742 5' similar to gb:M14219 BONE PROTEOGLYCAN II PRECURSOR
            (HUMAN).; mRNA sequence.
ACCESSION   H12824
NID   g877644
VERSION   H12824.1 GI:877644
KEYWORDS   EST.
SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 336)
AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
TITLE   The WashU-Merck EST Project
JOURNAL   Unpublished (1995)
COMMENT

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 814
High quality sequence stops: 284
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 814   Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 340.

FEATURES   Location/Qualifiers
     source   1..336
                     /organism="Homo sapiens"
                     /db_xref="GDB:560540"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:148742"
                     /clone_lib="Soares placenta Nb2HP"
                     /sex="Female"
                     /dev_stage="placenta obtained at birth (full term)"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     AACTGGAAGAATTCGCGGCCGCCGAGGAATTTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT   92 a   79 c   78 g   87 t
ORIGIN

alignment_scores:
        Quality: 7.00   Length: 7
        Ratio: 1.000   Gaps: 0
Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
US-09-092-297-17 x H12824/rev   .

Align seg 1/1 to reverse of: H12824   from: 1 to: 336

         40 TyrIleuMetLeuCysGlnPro 46
            |||||||||||||||||||||||
        319 TACTTAAYGCTCTGCCAGCCC 299

seq_name: gb_est3:R48084

seq_documentation_block:
LOCUS   R48084   465 bp   mRNA   EST   18-MAY-1995
DEFINITION yj63c02.r1 Soares breast 2NbHBst Homo sapiens cDNA clone
            IMAGE:153410 5' similar to gb:M62403 INSULIN-LIKE GROWTH FACTOR
            BINDING PROTEIN 4 PRECURSOR (HUMAN).; mRNA sequence.
ACCESSION   R48084
NID   g810110
VERSION   R48084.1 GI:810110
KEYWORDS   EST.
SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 465)
AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
TITLE   The WashU-Merck EST Project

```
JOURNAL     Unpublished (1995)
COMMENT     On Oct 24, 1994 this sequence version replaced.

            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 1309
            High quality sequence stops: 321 Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1309   Std Error: 0.00
            Seq primer: M13RP1
            High quality sequence stop: 321.
FEATURES             Location/Qualifiers
     source          1..465
                     /organism="Homo sapiens"
                     /db_xref="GDB:565726"
                     /db_xref="taxon:9606"
                     /map="8; 3 q25-q26"
                     /clone="IMAGE:153410"
                     /clone_lib="Soares breast 2NbHBst"
                     /sex="Female"
                     /dev_stage="adult"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: breast; Vector: pT73D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGAGGAGGCGGCGCGCCCCTTTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of a modified pT73 vector (Pharmacia).
                     Library went through one round of normalization to a Cot =
                     230. Library constructed by Bento Soares and M.Fatima
                     Bonaldo."
BASE COUNT      99 a    141 c    149 g    72 t    4 others
ORIGIN

alignment_scores:
             Quality:        7.00
             Ratio:          1.000
Percent Similarity: 100.000        Percent Identity: 100.000

alignment_block:
r--09-092-297-17 x R48084

. Jn seg 1/1  to: R48084   from: 1  to: 465

   32 AlaProValAlaProMetThr 38
      |||||||||||||||||||||||
   70 GCCCCTGTACCGCCCCATGACC 90

seq_name: gb_est3:R67627
```

```
             TITLE
             JOURNAL     Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                         Wilson,R.
                         The WashU-Merck EST Project
                         Unpublished (1995)
             COMMENT     On Sep 21, 1992 this sequence version replaced gi:276059.

                         Contact: Wilson RK
                         Washington University School of Medicine
                         4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                         Tel: 314 286 1800
                         Fax: 314 286 1810
                         Email: est@watson.wustl.edu
                         Insert Size: 916
                         High quality sequence stops: 230 Source: IMAGE Consortium, LLNL
                         This clone is available royalty-free through LLNL ; contact the
                         IMAGE Consortium (info@image.llnl.gov) for further information.
                         Insert Length: 916   Std Error: 0.00
                         Seq primer: Promega -21m13
                         High quality sequence stop: 230.
             FEATURES             Location/Qualifiers
                  source          1..474
                                  /organism="Homo sapiens"
                                  /db_xref="GDB:566386"
                                  /db_xref="taxon:9606"
                                  /clone="IMAGE:154004"
                                  /clone_lib="Soares breast 2NbHBst"
                                  /sex="Female"
                                  /dev_stage="adult"
                                  /lab_host="DH10B (ampicillin resistant)"
                                  /note="Organ: breast; Vector: pT73D (Pharmacia) with a
                                  modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                                  strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                  TGTTACCAATCTGAAGTGGGGAGGCGGCGCGCCCCTTTTTTTTTTTTTTTTTTTT 3'],
                                  double-stranded cDNA was ligated to Eco RI adaptors
                                  (Pharmacia), digested with Not I and cloned into the Not I
                                  and Eco RI sites of a modified pT73 vector (Pharmacia).
                                  Library went through one round of normalization to a Cot =
                                  230. Library constructed by Bento Soares and M.Fatima
                                  Bonaldo."
             BASE COUNT     107 a    112 c    131 g    114 t    10 others
             ORIGIN

             alignment_scores:
                          Quality:        7.00
                          Ratio:          1.000
             Percent Similarity: 100.000        Percent Identity: 100.000

             alignment_block:
             US-09-092-297-17 x R67627

             Align seq 1/1  to reverse of: R67627/rev    from: 1  to: 474

                1 ProLeuGlnProProArgAla 7
                  ||||||||||||||||||||||
              401 CCGCTGCAACCCCTCGGGGCT 381
```

```
seq_documentation_block:
LOCUS       R67627       474 bp    mRNA            EST       30-MAY-1995
DEFINITION  yi69c11.s1 Soares breast 2NbHBst Homo sapiens cDNA clone
            IMAGE:154004 3', mRNA sequence.
ACCESSION   R67627
NID         g840265
VERSION     R67627.1  GI:840265
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 474)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
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